Table 5: **Protease**

| | MAb ID | HXB2 Location | Author's Location | Sequence | Neutralizing | Immunogen | Species (Isotype) |
|---|---|---|---|---|---|---|---|
| 162 | 1696 | Protease(1–7) | Pro(1–7 BH10) | PQIYLWQ | | Vaccine | murine(IgG) |
| | ***Vaccine:*** | *Vector/type:* protein | *HIV component:* Protease | | | | |
| | | **Ab type:** N-term | **References:** [Lescar (1999)] | | | | |
| | | • 1696: MAb binds to HIV-1 and HIV-2, putative epitopes are PQIYLWQ and PQFSLWK respectively – Pro1 is critical, QIYLWQR residues 2–8 do not compete without it – MAb disrupts catalytic activity – crystal structure of Fab at 3 A resolution reveals a deep cavity lined by acidic and hydrophobic residues – the binding region is located within the region required for dimerization and the Fab structure could serve as a basis for drug design targeting this region [Lescar (1999)] | | | | | |
| 163 | 10E7 | Protease(36–46) | Pro(38–45 HXB2) | MSLPGRWKPKM | no | Vaccine | hamster(IgG) |
| | ***Vaccine:*** | *Vector/type:* recombinant protein | *HIV component:* Protease | | | | |
| | | **References:** [Croix (1993)] | | | | | |
| | | • 10E7: Immunodominant region of protease in Armenian hamster (but only weakly reactive in people, see: [Bjorling1992]) – peptide MSLPGRWKP blocks protease binding [Croix (1993)] | | | | | |
| 164 | F11.2.32 | Protease(36–46) | Pro(36–46 BH10) | MSLPGRWKPKM | | Vaccine | murine(IgG1$\kappa$) |
| | ***Vaccine:*** | *Vector/type:* recombinant protein | *Strain:* BH10 | *HIV component:* Protease | | | |
| | | **Ab type:** flap region | **References:** [Lescar (1996), Lescar (1997), Lescar (1999)] | | | | |
| | | • F11.2.32: Binding leads to significant inhibition in proteolytic activity – crystal structure of Fab-peptide was determined to 2.2 A resolution – bound peptide shows no structural similarity to the corresponding segment in native protease suggesting binding may distort protein structure [Lescar (1997)] | | | | | |
| | | • F11.2.32: Distortion may occur in the flap region of the protein, important for regulating access of substrate to the catalytic site [Lescar (1999)] | | | | | |
| 165 | 13E1 | Protease(38–45) | Pro(38–45 HXB2) | LPGRWKPK | no | Vaccine | hamster(IgG) |
| | ***Vaccine:*** | *Vector/type:* recombinant protein | *HIV component:* Protease | | | | |
| | | **References:** [Croix (1993)] | | | | | |
| | | • 13E1: LPGRWKPK is the core of the eptiope – binds to MSLPGRWKPKM with sightly higher affinity [Croix (1993)] | | | | | |
| 166 | 8B11 | Protease(38–45) | Pro(38–45 HXB2) | LPGRWKPK | no | Vaccine | hamster(IgG) |
| | ***Vaccine:*** | *Vector/type:* recombinant protein | *HIV component:* Protease | | | | |
| | | **References:** [Croix (1993)] | | | | | |
| | | • 8B11: LPGRWKPK is the core of the eptiope – binds to MSLPGRWKPKM with sightly higher affinity [Croix (1993)] | | | | | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 167 | 8C10 | Protease(38–45) | Pro(38–45 HXB2) | LPGRWKPK | no | Vaccine | hamster(IgG) |

***Vaccine:*** *Vector/type:* recombinant protein *HIV component:* Protease

**References:** [Croix (1993)]

- 8C10: LPGRWKPK is the core of the eptiope – binds to MSLPGRWKPKM with sightly higher affinity [Croix (1993)]

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 168 | 8G5 | Protease(38–45) | Pro(38–45 HXB2) | LPGRWKPK | no | Vaccine | hamster(IgG) |

***Vaccine:*** *Vector/type:* recombinant protein *HIV component:* Protease

**References:** [Croix (1993)]

- 8G5: LPGRWKPK is the core of the eptiope – binds to MSLPGRWKPKM with sightly higher affinity [Croix (1993)]